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Software version 6.1.3.4

protein BLAST v2.1
1.3 beta (Julian 3/97)

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Compaq server 1.4.4

protein BLAST v2.1
1.3 beta (Julian 3/97)

com protein protein search, using sw model

POST processing: Minimum Match 0.8

Perfect Score: 51

Sequence: 1 VQGRIR 6

Scoring table: BLASTNG2

Gapped 10.0 , Gapext 0.5

Searched:

total number of hits satisfying chosen parameters: 288138

Minimum DB seq length: 0

Maximum DB seq length: 20000000

POST processing: Minimum Match 0.8

Maximum Match 1000

listing first 4% summaries

database : PIR_71;*

1: p1r1;*

2: p1r2;*

3: p1r3;*

4: p1r4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS 1

1: 43720

hypothetical 12-4K protein - Escherichia coli

No Alternative names: hypothetical protein 114

Comments: Escherichia coli

Accession: CAA5720

Reference: C.B., Yoo, D.Z., Zhou, Z., Warner, B.L., Walsh, C.T., J. Biol. Chem., 265, 4461-4471, 1990

Alt ID(s): M66619; Biology of carbon phosphate bond cleavage, Cloning and sequencing

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 1:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

2: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 2:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

3: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 3:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

4: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 4:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

5: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 5:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

6: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 6:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

7: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 7:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

8: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 8:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

9: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 9:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

10: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 10:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

11: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 11:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

12: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 12:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

13: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 13:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Coverage: 66%

Start codon: ATG

c: Superfamily: Escherichia coli hypothetical 12-4K protein

RESULTS 1

14: 100,000

hypothetical protein

No Alternative names: hypothetical protein

Comments: Autobacterium thermophilic

Accession: CAA5720

Reference: C.B., Hunter, G.J., Gartland, S.J., Miller, S., Belmonte, M., control, H., Saito, T., Lopez, C., Berkner,

A., Berkner, K., Williams, C., Allardice, R., 2001

Accession Number: A55718; M01070170953

Accession Type: PIA

Accessions: 14:114-CHI

Access reference: CAA5720; M1501471; P10N AAAA3V1; 1:2 1111:6455163

Molecule Type: DNA
 Residues: 1-269, SCH
 Cross-references: 1993-AF093972, 911-43794193, PDB-1C9A, PDB-1C9B
 Query Match: 96.8%; Scores: 602/642; Length: 269
 Best local Similarity: 84.3%; Pred. No.: 74; Mismatches: 13
 Matches: 114; Conserved: 114; Deletions: 13; Insertions: 13
 1. VORICK, G.
 11111
 55 10000 66

Molecule type: DNA
 Residues: 1-694, SCH
 Cross-references: 1993; AP0083972; S10415793; S10415794; S10415795; S10415796; S10415797; S10415798; S10415799; S10415800
 Query Match: 96.8%; Score: 90; Id: Benth 209;
 Best local Similarity: 84.3%;
 Matches: 51;保守性匹配: 17; M:SMART: 0%; T: SMART: 0%; V: SMART: 0%;
 Amino acid sequence:
 1 VQEGK 6
 11111
 55 IQRMV 60
 56)

Accession number: Z16628
Status: preliminary; translated from "B2390799"
Molecule type: mRNA
Residues: 1-141 (W)
Cross-references: EMBL:X66738; MIR:3124750;
Experimental source: isolate A; Phytocromes: Phytochrome homology
Superfamily: phytochrome; photoreceptor; phytochromobilin
Keywords: chlorophotoprotein; phytochrome; hematology; phytochrome; phytochromobilin
Organism: *Arabidopsis thaliana*; Plantae; Marchantiophyta; vascular plant; predicted

Query	Match	Score	for 2;	Length	11-11;		
		Pred.	No. 2, etc., etc.	Mismatches	0;	Gaps	(1)
Best local Similarity	94.8%	Score 307	for 2;	Length 11-11;			
Matches	55;	Pred.	No. 2, etc., etc.	Mismatches	0;	Gaps	(1)
Conservative	93.8%						
1. FOREIGN	6						
82. FOREIGN	87						

9156
SUSU 19
proteotypical protein in MTH430 - Methanobacterium thermoadaptrophicum (strain 161)
Species: Methanobacterium thermoadaptrophicum
Isolate: 05 Dec 1997 #sequence-revision
Accession #: B66556
Smith, D. R.; Deutscher-Stamm, L. A.; McLoud, H. J.; Lubinoff, J.; Aldrich, C. S.; Ong, K.; Spadaro, R.; Vitiello, R.; Ward, V.; Wier-Lawlor, J.; Williams, R.; Church, G. M.; Daniels, C. J.; Mao, J.; Rice, P.; Revitt, D.; Revett, J. Bacteriol., 179, 7145-7155, 1997

Title: Complete genome sequence of *Wolbachia* *temulentum* thermophilum of *Platynereis dumerilii*
 Reference number: A69000; M010298037514
 Accession: B669156
 Status: Preliminary
 Molecule type: DNA
 Residues: 1-141, 86H
 Expressor: *Wolbachia* sp. *Anthonomus* sp., 331342524492, 171446743739, 171446743739, 171446743739
 Experimental source: strain *Pd1a H*
 Genotypes:
 Gene: *WolbA* 80
 Start codon: TGG
 Stop codon: TGG

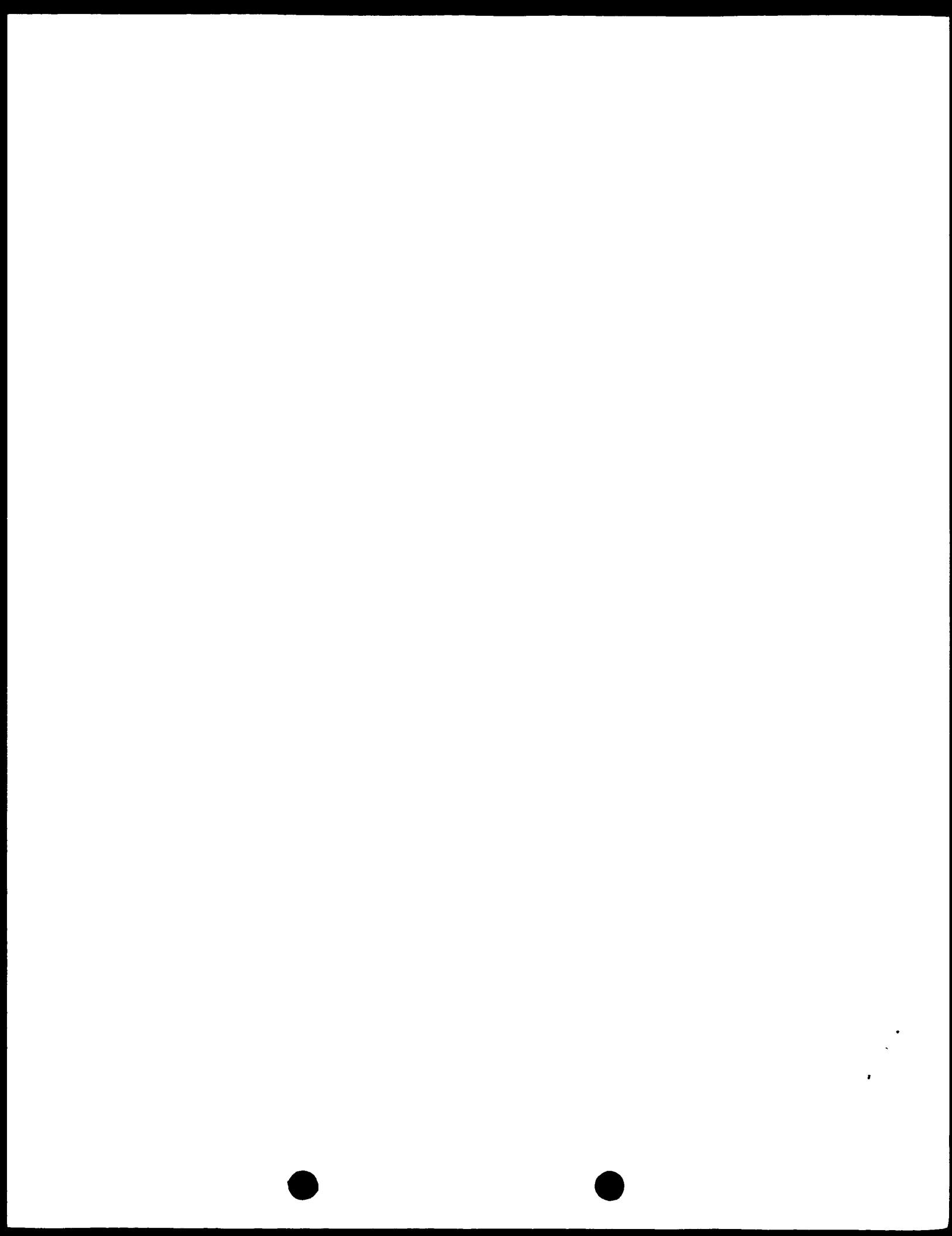
Query Match	90.36%	Score: 28	DB2	Length: 44
Best Local Similarity	83.38%	Prod. No.	1.1e-02	
Conservative	1.0	Minmatch	0.0	
Matches	1	Maxmatch	1.0	
		Maxgap	1.0	

Tue Oct 22 17:41:08 2002

us-09-996-738-8.rpr

Page 5

JAIL TIME : 4.0982 SECS



Result No.	Score	Query	Match Length	DB ID	Description
1	31	100.0	567	1	MEI_SCHPO
2	41	100.0	1151	1	HAI_HUMAN
3	40	96.8	1131	1	PHY_PENNY
4	28	90.3	235	1	CSPN_ISPAE
5	24	90.3	281	1	DESV_BACSU
6	23	90.4	425	1	VIF6_RTV15
7	29	90.2	325	1	VIF6_BTVEL1
8	23	90.3	325	1	VIF6_BTVEL2
9	28	90.3	429	1	VIF6_JMV10
10	28	90.3	376	1	KTH_ISV28
11	28	90.3	650	1	PHM_ISV31
12	28	90.3	882	1	HRV_31V01
13	29	87.1	88	1	R015_BRANA
14	27	87.1	153	1	R015_BRIG
15	27	87.1	164	1	R015_BRAS1
16	27	87.1	165	1	R015_CHICK
17	27	87.1	173	1	FRI2_RANCA
18	27	87.1	174	1	FRIH_BIVIN
19	27	87.1	174	1	FRIH_BORSE
20	27	87.1	174	1	FRIH_BURMAN
21	27	87.1	174	1	FRIH_BRAUL
22	27	87.1	177	1	FRIH_GALSA
23	27	87.1	179	1	FRIH_CHICK
24	27	87.1	180	1	FRIH_BIVIN
25	27	87.1	181	1	FRIH_MOUSE
26	27	87.1	181	1	FRIH_RAT
27	27	87.1	182	1	FRIH_HUMAN
28	27	87.1	182	1	FRIH_TREVII
29	27	87.1	185	1	SREB2_SNMP7
30	27	87.1	185	1	FRIH_BIRTR
31	27	87.1	174	1	R15F_VKAB
32	27	87.1	174	1	R15F_DYKHO
33	27	87.1	174	1	R15_SCHHE

Scoring table:
BLASTP62
gapop 10.0 , Gapext 0.5

Scanned:
105224 seqs, 4871950 residues

Total number of hits satisfying chosen parameters: 109244

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 0%

Displaying first 45 summaries

Database : Swissprot_40;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the test set being printed, and is derived by₂ analysis of the total score distribution.

SUMMARY

Query Score: 90.3

Result No.: 1

Score: 100.0

Match Length: 567

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 566

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 565

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 564

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 563

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 562

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 561

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 560

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 559

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 558

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 557

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 556

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 555

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 554

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 553

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 552

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 551

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 550

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 549

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 548

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 547

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 546

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 545

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 544

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 543

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 542

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 541

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 540

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 539

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 538

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 537

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 536

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 535

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 534

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 533

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 532

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 531

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 530

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 529

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 528

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 527

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 526

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 525

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 524

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 523

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 522

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 521

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 520

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 519

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 518

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Match Length: 517

DB ID: 1

Description: schizosaccharomyces pombe (fission yeast).

Score: 99.9

Bennet D.J., Yand M., Ferrari E.: A mutagenization of *Bacillus subtilis* sacB(BY) mutations to two linked components with facilitating to the classical presecretory family of two component signalling systems." J. Bacteriol. 170:5102-5109 (1988).

-!- SIMILARITY: USES S-AAPPEL-PASCAL-EXP1-AVANTPROTEIN_15.5_EA_PEG1H (AC P13977) AND TO B_GUSTAVSEN_RG_P6.

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EMBL: 218629; CAA79225; 1;
 EMBL: 056901; AAC44939; 1;
 EMBL: M23559; PDB_ARBITRATOR_CDS;
 EMBL: 2599122; CAB5565; 1;
 PIR: D30191; D30191;
 PIR: S28536; S28536;
 Subfam: Subfam_B01394; desy_V;
 InterPro: IPR003797; DUF194; 1;
 Pfam: PF02645; DUF194; 1;
 Complete Protein_Co:
 Spfamily: 21690; MW: 72770; pI: 5.47; length: 147;

Query Match: 90.3%; Score: 28; DB: 1; Length: 281;
 Best Local Similarity: 87.3%; Prod: 59.7%;
 Matches: 1; Conserv: 1; Minmatch: 56.5%;
 0.; Gaps: 0.; Gaps: 0.;

1 VPGGP 6
 :11111
 167 LQRLSER 172

SUPERFAMILY: 6
 VP6_BPV1 STANDARD: PRT: 325 AA.
 P32933; 01-OCT-1993 (Rev: 27, Created)
 01-OCT-1993 (Rev: 27, Last sequence update)
 15-OCT-1998 (Rev: 37, Last annotation update)
 VP6 protein (Minor inner core protein VP6).
 S9.1
 blue-orange virus (serotype 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 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1859, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1886, 1887, 1888, 1889, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1895, 1896, 1897, 1898, 1899, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1949, 195

15 Dec 1998 (Ref.: 37, Last annotation update)
Vp6 protein (Minor, later one produced via e-mail)

DE
SGN
BLASTn (evalue: 7.7e-13, censored by user)
Viruses: dsDNA viruses, Eukaryotes, eukaryotes
NBL: TaxD 47743

LN

SR

SP SEQUENCE FROM N.A.
ML MEDLINE 94043709, Published 1994-07-11

RA Baojun G., Yee-chun J., Fan-Y., Li J.-K., K.-J.
RE Comparative sequence analyses of the coat protein products Vp6,
RI "comparative sequence analyses of the coat protein products Vp6,
RI of BTV-13, BTV-14 and BTV-15",
RI Virus Res. 24:415-323(1992).

RC FUNCTION: SPARKLES AND INTERACTS WITH THE GENE 3152 AG RNA,
RC POSSESSES SS- AND DS-BINDING CAPACITY, ITS HYDROPHOBIC
RC NATURE AND AVAILABILITY: THE BTV-13 AND BTV-14 COAT PROTEIN
RC INTERACTIONS WITH BTV GENOMIC RNA.

RC SUBCELLULAR LOCATION: INNER CAPSID.

RC SIMILARITY: BELONGS TO THE REOVIRUSES Vp6 FAMILY.

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EMBL: L09672; AAA2821; 1;

PRINTS: PF01516; orb1_VP6; 1; core protein; PRO0902; VP6RAFTID;	
KW DOMAIN	
SEQUENCE: 425 AA: 84 125 GLY RICH	
6E175986AZHAA1411 Rev.4;	
Query Match Score: 28.2 / 103.4; Length: 327;	
Best Local Similarity: 83.4%; Pred. No.: 67.7;	
Matches: 57; Conservativeness: 12; Mismatches: 0; Indels: 0; Gaps: 0;	
WS 1 V06GR 6	
16 149 VEROGR z04	
RESULT: 9	
VP6_BTIV10	
STANDARD:	
PR1: 329 Å.	
PR0166; PR	
01-NOV-1991 (Ref.: 20, Created)	
01-FEB-1996 (Ref.: 33, Last Sequence Update)	
15-DEC-1998 (Ref.: 37, Last Annotation Update)	
VP6 protein (Minor inner core protein VP6) (Version 1),	
GN S99	
BLASTN search (core protein VP6) (version 5),	
Viruses: dsDNA viruses; possiviridae; orbivirus;	
NCBI_TaxID: 10906;	
RN 11	
SEQUENCE FROM N.A.	
MATERIAL: B9294376; 1436.d; 2546633;	
Fukasho A., Yu Y., Yamamoto S., Kuroki T.,	
"completion of the sequence of bluetongue virus serotype 10 by the characterization of a structural protein, VP6, and a non structural	
protein, NS2,"	
J. Gen. Virol., 70:1677-1689(1989).	
RN 121	
SEQUENCE FROM N.A.	
MEDLINE: 90435726; Published 2/16/649;	
ROY P., MARSHALL J.D. A., French T.,	
"Structure of the bluetongue virus genome and its extended protein,"	
Cure, Top. Microbiol. Immunol., 162:43-87 (1991).	
REV. 13	
RP	

RESULT 1	KL15_BRANA	STANDARD:	PRT:
0Y	1	W05038 6	
(ab)	8559	L05038 6	
Best local Similarity	95.3%	95.3%	95.3%
Matches	8433k	9433k	9433k
% Conservative	1.2	1.2	1.2
Mismatches	0	0	0
Nodes	548	548	548
Ref ID	R15_BRANA	R15_BRANA	R15_BRANA
Ref No	P4-289;	P4-289;	P4-289;
Ref Rev	32	32	32
Ref DT	01-Nov-1995	01-Nov-1995	01-Nov-1995
Ref Desc	last sequence update	last sequence update	last sequence update

KW	Ribosomal protein.	STANDARD:	PRT:	Matched:	%	Conservative:	%	Mismatches:	%	Indels:	%	Unps:	%
FI	NON_TER	1	1	1	100	100	100	0	0	0	0	0	0
SK	STRUCTURE_P	154 AA.	154 AA.	154	100	100	100	0	0	0	0	0	0
Query Match	87.1%	Score: 273	108 14	273	100	100	100	0	0	0	0	0	0
Best Local Similarity	83.4%	Freq. No. 55;	Length 153;	153	100	100	100	0	0	0	0	0	0
Matches	5;	Conservative	0;	0	0	0	0	0	0	0	0	0	0
OF	Ferritin heavy chain (Ferritin H subunit) (Fragment).	15-JUL-1999 (Ref. 38; last annotation update)	15-JUL-1999 (Ref. 22; last sequence update)	15-JUL-1999 (Ref. 22; last sequence update)	100	100	100	0	0	0	0	0	0
GN	FTH.				100	100	100	0	0	0	0	0	0
OS	Oryctolagus cuniculus (Rabbit).				100	100	100	0	0	0	0	0	0
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:				100	100	100	0	0	0	0	0	0
OM	Mammalia: Eutheria: Laurasiatheria: Eutherian mammals: Oryctolagans:				100	100	100	0	0	0	0	0	0
OX	NCBI-TaxID: 9986;				100	100	100	0	0	0	0	0	0
RN	111				100	100	100	0	0	0	0	0	0
RP	SEQUENCE FIRM: N_A.				100	100	100	0	0	0	0	0	0
RC	TISSUE: Vascular smooth muscle;				100	100	100	0	0	0	0	0	0
RX	PMID:11647; PubMed:655764;				100	100	100	0	0	0	0	0	0
RA	Liu G., Chan L. M., Feng P.;				100	100	100	0	0	0	0	0	0
RT	"increased ferritin gene expression is both promoted by cAMP and a marker of growth arrest in rabbit vascular smooth muscle cells."				100	100	100	0	0	0	0	0	0
RL	J. Biol. Chem. 266:18819-18826(1991).				100	100	100	0	0	0	0	0	0
CC	-1- FUNCTION: FERRITIN IS AN INTERFACE-LIKE PROTEIN THAT STORES IRON IN A SOLUBLE, NONTOXIC, READILY AVAILABLE FORM. THE FUNCTIONAL MOLECULE, WHICH IS COMPOSED OF 24 CHAINS, IS ROUGHLY SPHERICAL AND CONTAINS A CENTRAL CAVITY IN WHICH THE POLYMERIC FERRIC IRON CORE IS DEPOSITED.				100	100	100	0	0	0	0	0	0
CC	-1- MISCELLANEOUS: THERE ARE TWO TYPES OF FERRITIN SUBUNITS: L (LIGHT) CHAIN AND H (HEAVY) CHAIN. THE MAJOR CHAIN CAN BE LIGHT OR HEAVY, DEPENDING ON THE SPECIES AND TISSUE TYPE.				100	100	100	0	0	0	0	0	0
CC	-1- SIMILARITY: BELONGS TO THE FERRITIN FAMILY.				100	100	100	0	0	0	0	0	0
CC	-----				100	100	100	0	0	0	0	0	0
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on behalf of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Use is made by and for commercial enterprises, however, with their permission or by arrangement with the EBI or send an email to license@ebi.ac.uk.				100	100	100	0	0	0	0	0	0
DR	EMBL: M63912; AA031247; 1;				100	100	100	0	0	0	0	0	0
DR	HSSP; P02794; 2BHA.				100	100	100	0	0	0	0	0	0
DR	InterPro: IPR001519; Ferritin.				100	100	100	0	0	0	0	0	0
DR	Pram: PF00210; ferritin_1.				100	100	100	0	0	0	0	0	0
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DR	PROSITE: PS002040; FERRITIN_2; 1.				100	100	100	0	0	0	0	0	0
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STRAIN-10M 1617 / p2:
 Chatelain R.L., Singh R.K., Chan-Wenget C.C., Allard G., Chow C.,
 Constanzer J.P., Curtis B.S., Dupper M., Frausto G., Fapuy B.,
 Gaasterland T., Garrett R.A., Gordon P., Jetters A.C., Kozeta C.,
 Kushwaha N., Lathe E., Medina N., Peña X., Penny S.L., Shi Z.,
 St. Jean A., Van Der Velde J., Young P., Zarando P., Rodriguez W.F.,
 Radan M.A., Sensen C.W.;
 Gene content and organization of a 281 kbp contig from the genomes of
 the extremely thermophilic archaeon, Sulfolobus solfataricus P2, submitted
 (APP-1617) to the [EMBL/Genbank/DBJ](http://www.ncbi.nlm.nih.gov) databases.

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MEDLINE 98423450; PubMed 974410;

Schaeffer C., Delmonte P.P., Prostroj N.M., Krishnam R.A., Wu K.Y.,

Scieszko B.V.;

"Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrotrophic archaeon *Candidatus symbiosum*,"

J. Bacteriol. 180:5003-5006 (1998).

EMBL AP084072; AAC662709; L1:

InterPro IPR004115; ParBc;

Protein families: *parBc*, *parBc*

Query Match 96.88; Score 40; IB 1; Length 269;
 Best Local Similarity 84.36; Prod. No. 947
 Matches 5; Consistency 1; Misclassification 0; Uncls. 0; Uncls. 0

STRAIN A:

query	batch	best local	similarity	Score	pred.	Rec.	length	units
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Salmones	q2	concentrative	86.98%	86.98	0.02	0.02	2.75	0.2
Salmones	q3	concentrative	71.83%	71.83	0.02	0.02	2.75	0.2
Salmones	q4	concentrative	68.33%	68.33	0.02	0.02	2.75	0.2
Salmones	q5	concentrative	66.67%	66.67	0.02	0.02	2.75	0.2
Salmones	q6	concentrative	65.00%	65.00	0.02	0.02	2.75	0.2
Salmones	q7	concentrative	63.33%	63.33	0.02	0.02	2.75	0.2
Salmones	q8	concentrative	61.67%	61.67	0.02	0.02	2.75	0.2
Salmones	q9	concentrative	60.00%	60.00	0.02	0.02	2.75	0.2
Salmones	q10	concentrative	58.33%	58.33	0.02	0.02	2.75	0.2
Salmones	q11	concentrative	56.67%	56.67	0.02	0.02	2.75	0.2
Salmones	q12	concentrative	55.00%	55.00	0.02	0.02	2.75	0.2
Salmones	q13	concentrative	53.33%	53.33	0.02	0.02	2.75	0.2
Salmones	q14	concentrative	51.67%	51.67	0.02	0.02	2.75	0.2
Salmones	q15	concentrative	50.00%	50.00	0.02	0.02	2.75	0.2
Salmones	q16	concentrative	48.33%	48.33	0.02	0.02	2.75	0.2
Salmones	q17	concentrative	46.67%	46.67	0.02	0.02	2.75	0.2
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Salmones	q19	concentrative	43.33%	43.33	0.02	0.02	2.75	0.2
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Salmones	q40	concentrative	8.33%	8.33	0.02	0.02	2.75	0.2
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Salmones	q42	concentrative	5.00%	5.00	0.02	0.02	2.75	0.2
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Salmones	q45	concentrative	0.00%	0.00	0.02	0.02	2.75	0.2

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PERSON	PER	Person	http://www.eionet.europa.eu/person	2003-06-03
PLACE	PLA	Place	http://www.eionet.europa.eu/place	2003-06-03
TIME	TEM	Time	http://www.eionet.europa.eu/time	2003-06-03
TOPIC	TOP	Topic	http://www.eionet.europa.eu/topic	2003-06-03
CONCEPT	CON	Concept	http://www.eionet.europa.eu/concept	2003-06-03
THEORY	THE	Theory	http://www.eionet.europa.eu/theory	2003-06-03
DATA	DAT	Data	http://www.eionet.europa.eu/data	2003-06-03
STANDARD	STD	Standard	http://www.eionet.europa.eu/standard	2003-06-03
DEFINITION	DEF	Definition	http://www.eionet.europa.eu/definition	2003-06-03
EXPLANATION	EXP	Explanation	http://www.eionet.europa.eu/explanation	2003-06-03
EXAMPLE	EXA	Example	http://www.eionet.europa.eu/example	2003-06-03
QUESTION	QUE	Question	http://www.eionet.europa.eu/question	2003-06-03
ANSWER	ANS	Answer	http://www.eionet.europa.eu/answer	2003-06-03
NOTATION	NOT	Notation	http://www.eionet.europa.eu/notation	2003-06-03
SCHEMATIC	SCHE	Schematic	http://www.eionet.europa.eu/schematic	2003-06-03
GRAPHICAL	GRAPH	Graphical	http://www.eionet.europa.eu/graphical	2003-06-03
ALGEBRAIC	ALG	Algebraic	http://www.eionet.europa.eu/algebraic	2003-06-03
LOGICAL	LOG	Logical	http://www.eionet.europa.eu/logical	2003-06-03
PHYSICAL	PHYS	Physical	http://www.eionet.europa.eu/physical	2003-06-03
MATERIAL	MAT	Material	http://www.eionet.europa.eu/material	2003-06-03
IDEAS	IDE	Ideas	http://www.eionet.europa.eu/ideas	2003-06-03
CHARACTERISTICS	CHAR	Characteristics	http://www.eionet.europa.eu/characteristics	2003-06-03

STRAIN A (2); Serrano A.M.; Parkhill J.; Barrell B.G.; Barlandam M.A.; Submitted (Friction) to the EMBO/Prokaryotic databases; Submitted (Friction) to the EMBL/Prokaryotic databases.

A Rodenbach M., Kieser H. M., Dennerlein D., Eichner A., Gullion J., Kutsch B., Hopwood J. A.: A set of ordered cosets and a detailed structure of physical quantities. *Structural coefficients $A(\zeta)$ of the octonion*, *J. Mol. Microbiol.* 21:77-96 (1996).

R Eichner A.: All octonionic representations of the Lie group G_2 . *Octonionic geometry*, *Proc. Roy. Irish Acad. Sect. A* 96(1):1-12 (1996).

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263	CD280	CD280	CD280
264	CD281	CD281	CD281
265	CD282	CD282	CD282
266	CD283	CD283	CD283
267	CD284	CD284	CD284
268	CD285	CD285	CD285
269	CD286	CD286	CD286
270	CD287	CD287	CD287
271	CD288	CD288	CD288
272	CD289	CD289	CD289
273	CD290	CD290	CD290
274	CD291	CD291	CD291
275	CD292	CD292	CD292
276	CD293	CD293	CD293
277	CD294	CD294	CD294
278	CD295	CD295	CD295
279	CD296	CD296	CD296
280	CD297	CD297	CD297
281	CD298	CD298	CD298
282	CD299	CD299	CD299
283	CD300	CD300	CD300
284	CD301	CD301	CD301
285	CD302	CD302	CD302
286	CD303	CD303	CD303
287	CD304	CD304	CD304
288	CD305	CD305	CD305
289	CD306	CD306	CD306
290	CD307	CD307	CD307
291	CD308	CD308	CD308
292	CD309	CD309	CD309
293	CD310	CD310	CD310
294	CD311	CD311	CD311
295	CD312	CD312	CD312
296	CD313	CD313	CD313
297	CD314	CD314	CD314
298	CD315	CD315	CD315
299	CD316	CD316	CD316
300	CD317	CD317	CD317
301	CD318	CD318	CD318
302	CD319	CD319	CD319
303	CD320	CD320	CD320
304	CD321	CD321	CD321
305	CD322	CD322	CD322
306	CD323	CD323	CD323
307	CD324	CD324	CD324
308	CD325	CD325	CD325
309	CD326	CD326	CD326
310	CD327	CD327	CD327
311	CD328	CD328	CD328
312	CD329	CD329	CD329
313	CD330	CD330	CD330
314	CD331	CD331	CD331
315	CD332	CD332	CD332
316	CD333	CD333	CD333
317	CD334	CD334	CD334
318	CD335		

STRAHAN A.(2);
SWEET R.J.; HARRIS D.J.;
CHAMBERS V.H.; TAYLOR J.L.;
SPAGHETTI B.M. N.A.
STRAHAN A.(2);
COTTER A.M.; PARKHILL J.; BARRELL
Submitted (this month) to the EMG/EMI

Romigkbach M., Kirsch H.M., Rehbari A., Kutsch H., Hopwood B.A.: A set of ordered cosets and a description of the structure of the Lie group $M_{\text{SL}}(M_{\text{SL}})$, *Z. für Physik* 21, 77-96 (1966).
E-mail: Rehbari@Physik.Uni-Bayreuth.DE.

	Accuracy	Recall	Specificity	Precision	F1	Mi
Gender Match	95.0%	95.0%	95.0%	95.0%	95.0%	95.0%
Best Local Similarity	84.9%	84.9%	84.9%	84.9%	84.9%	84.9%
Matches	82.0%	82.0%	82.0%	82.0%	82.0%	82.0%
Classification	82.0%	82.0%	82.0%	82.0%	82.0%	82.0%
Y	1.0	1.0	1.0	1.0	1.0	1.0
N	1.0	1.0	1.0	1.0	1.0	1.0
1	1.0	1.0	1.0	1.0	1.0	1.0
0	1.0	1.0	1.0	1.0	1.0	1.0
0.5	1.0	1.0	1.0	1.0	1.0	1.0

INTRODUCTION

S. M. Friedman R. A. Wu K. V. Patel
Evaluation of natural perforated
charcoal charcoons stain removal.

3.4.4: An implementation of the `update()` method for the `DA` class:

```

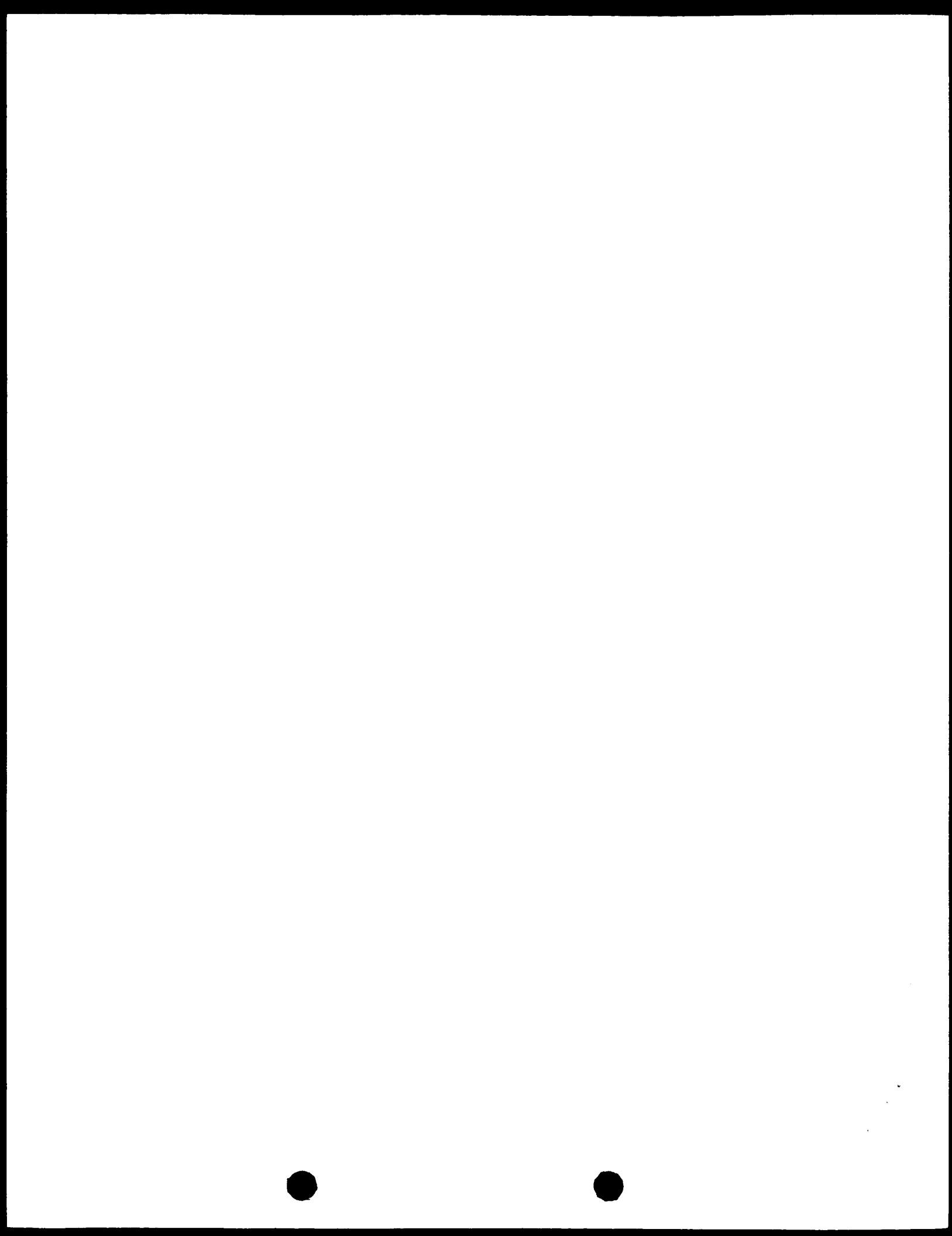
    public void update() {
        if (this.isFull) {
            System.out.println("The DA is full");
        } else {
            System.out.println("The DA has " + this.size + " elements");
        }
    }

```

The Dr. Richter A., William J.,
Detailed descriptive and physical m-
aterials, some 750 pages.

standard class

I.2. AN.



Result No.	Score	Query Match length	Depth	Annotation	Description	Protein ID	Protein Name	Species	Organism	Protein Function	Protein Interaction
1	41	100.0	6	22	ABY85004.3					Human alpha1 integrin	
2	41	100.0	14.8	22	ABY85004.3					Human fibroblast extracellular matrix receptor	
3	41	100.0	14.8	22	ABY85004.3					Human fibroblast extracellular matrix receptor	
4	41	100.0	20.6	22	ABY85004.3					Human fibroblast extracellular matrix receptor	
5	41	100.0	21.4	22	ABY85004.3					Human fibroblast extracellular matrix receptor	
6	41	100.0	37.8	22	ABY85004.3					Propionibacterium	
7	41	100.0	75.5	22	ABY85004.3					Propionibacterium	
8	41	100.0	118.8	22	ABY85004.3					Acinetobacter baumannii	
9	40	96.8	45	17	ABR8744.1					Synthetic HIV protein	
10	40	96.8	26.9	21	ABY85004.3					Cyanobacterial symbiont	
11	40	96.8	27.3	21	ABY85004.3					Cyanobacterial symbiont	

Result!	No.	Subqueries			Description
		Score	Match Length	DB	
4	1	100.0	6	22	AB85004.8
	2	100.0	148	22	AB85004.4
	3	100.0	148	22	AB85004.4
	4	100.0	206	22	AB85004.5
	5	100.0	214	22	AB85004.2
	6	100.0	338	22	AB85004.7
	7	100.0	755	22	AB85004.4
	8	100.0	1183	20	AB85004.3
	9	96.8	35	17	ABR874.1
	10	96.8	269	21	ABY9004.3
	11	96.8	273	21	ABY9004.9

VIA-1 for treating inflammatory disorders, in particular arthritis

Claim 1: FIG 15; 60P: English.

The present invention relates to the use of an anti-histatinal function blocking agent in the treatment of inflammatory diseases, in particular domain (VIA-1). The antibody of the present invention is useful for treating as inflammatory disorder e.g. rheumatoid arthritis, psoriasis, acne, eczema, rosacea, lichen nod., joint, asthma, bronchitis, menstrual cramps, tendinitis, bursitis, and the treatment of pain and headaches, or as an antipyretic, for the treatment of fever, gastrointestinal conditions such as inflammatory bowel diseases, Crohn's disease, gastritis and vascular diseases, migraine, headaches, tinnitus, tinea cap., dermatitis, urticaria, anaemia, hypertension, rheumatic fever, type I diabetes, myasthenia gravis, multiple sclerosis, sarcoidosis, nephritic syndrome, myocardial ischaemia, allergic rhinitis, respiratory distress syndrome, and/or chronic sinusitis and other diseases.

卷之三

Mai 19

Local Similarities

ט' ט' ט'

卷之三

2

ANALYSIS

All 196 34:

M - DEUTSCHE

CONTINUITY; CONTINUANCE

卷之三

hyperspace

卷之三

CENSUS PAPERS

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卷之三

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1. - MAK - 2000; 2000;

2000 : 2000

卷之三十一

0002-1000-0111-0

27-JUL-2000; 20000

melanomas, neoplasms of the breast or liver, septicemic sinusitis, and Gaucher's disease), neurological diseases (e.g., Alzheimer's disease, Parkinson's disease, encephalitis, cerebral abscesses), disorders of cardiac arrest, tachyarrhythmia and arrhythmia, infections caused by bacteria, viruses and fungi, and ocular disorders (e.g., congenital cataracts). Other uses include wound repair, maintenance of organs before transplantation.

specimens were obtained in effect from Germany from which
it was published for the first time.

Query Match	Score	Length	Length
Best local Similarity	100.0%	142	148
Matches	6	0	0
Consonantige	100.0%	100.0%	100.0%
Mismatches	0	0	0
Indels	0	0	0
Gaps	0	0	0

XX
11. 1 A MARK ZEOLITE (LITUS-zeolite)

AA DE Human alveolar interstitium
XX XX

X teach supplement; medical imaging; diagnostic; genetic disorder; KW vascular disease; autoimmune; respiratory distress syndrome; endotoxin shock syndrome; heterotaxy.

W₂O₁₇5.067 Å₂.
N X
HgBr₂ - Sample S.
XX
XX

--

Wojciechowski, M., 2001. *Geographic distribution of the species of the genus *Leptothrix* (Diptera, Streblidae) in Poland*. *Acta Biologica Cracoviensia*, 43(2), 1-10.

N-TERM: RASV422. X New isolated polynucleotide and ciliated polyribosomes, useful in use of blocking monovalent antibody capable of binding to an epitope of **WPL: 2601 06448/01.**

PLA 1 for treating inflammatory disorders, in particular arthritis, diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess bioterrorism.

The present invention relates to the use of an alpha-helical function as a model for peptide antibiotics.

The invention relates to isolated polyguanidine (1) and polyguanidine (1') sequences, (1) is useful as hybridisation probes, (VIA 1), and (1') is useful as hybridisation probes, (VIA 2).

skin related conditions such as psoriasis, eczema, burns and dermatitis, acne, bacterial, fungal and viral infections, menstrual cramps, tendinitis, tendonitis, carpal tunnel syndrome, and the like.

concerned with the diagnosis and treatment of diseases of the heart and blood vessels.

(11), (11) is useful for generating antibodies against it, developing or quantitating a polypeptide in tissue as well as in whole markers and as a food supplement. (11) and its binding partners are useful in medical diagnostics, particularly thyroiditis, apathy, depression, Cushing's syndrome, thrombotic stroke, The diabetics, myocardial infarction, multiple sclerosis, sarcoidosis, nephrotic syndrome, myocardial

ischemic, atopic rhinitis, respiratory distress syndrome, endotracheal intubation, and atelectasis. The present sequence is the human immunodeficiency virus-associated disease.

The porphyric and bonvivante species can have different expressions of diadromosis, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity. The optimal tool will depend on the sequence.

and to produce other types of data and products dependent on DNA and amino acid sequences. Abgenosys ARG30377 represent novel human diagnostic amino acid sequences of the invention.

QY 1 VQREGR 6
ID AAU47587 standard protein, 378 AA.
XX
AC AAU47587;
XX
DT 27-APR-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #6488.
XX
KW Sarcoidosis; granulomatosis; acne; folliculitis; bacterioses; comedones; cellulitis; vesiculitis; endophthalmitis; bone joint; central nervous system; ELISA; inflammatory lesions; cutaneous; mucous membranes; skin; acne vulgaris; dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO2001181581-A2.
XX
PD 01-NW-2001.
XX
PF 20-APR-2001; 2001WO-01812965.
XX
PR 21-APR-2000; 2000US199047P.
PR 02-JUN-2000; 2000US198841P.
PR 07-JUL-2000; 2000US1216747P.
XX
PA (CORI) CORIWA GMBH.
XX
P1 Skolnick YAV, Porat YY, Miriam M, Witztum J, Phatia A;
P1 L'Amisaneau J, Zhang Y, Jen S, Carter L;
XX
DP 2001-01-12-2001.
DB NPSB: AAS0553.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
vaccinating against and diagnosing infections, especially acne vulgaris -
PT treating acne vulgaris -
XX
SS

RESULT 6

AAU47587
ID AAU47587 standard protein, 378 AA.
XX
AC AAU47587;
XX
DT 27-APR-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #6488.

XX
KW Sarcoidosis; granulomatosis; acne; folliculitis; bacterioses; comedones; cellulitis; vesiculitis; endophthalmitis; bone joint; central nervous system; ELISA; inflammatory lesions; cutaneous; mucous membranes; skin; acne vulgaris; dermatological; osteopathic; neuroprotectant.

XX
OS Propionibacterium acnes.

XX
PN WO2001181581-A2.

XX
PD 01-NW-2001.

XX
PF 20-APR-2001; 2001WO-01812965.

XX
PR 21-APR-2000; 2000US199047P.

PR 02-JUN-2000; 2000US198841P.

PR 07-JUL-2000; 2000US1216747P.

XX
PA (CORI) CORIWA GMBH.

XX
P1 Skolnick YAV, Porat YY, Miriam M, Witztum J, Phatia A;

P1 L'Amisaneau J, Zhang Y, Jen S, Carter L;

XX
DP 2001-01-12-2001.

DB NPSB: AAS0553.

XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
vaccinating against and diagnosing infections, especially acne vulgaris -
PT treating acne vulgaris -

XX
SS

Example 1: SEQ ID: NC_87823; 1064BP; Unpublished.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment of acne vulgaris and lesions caused by *P. acnes*. The disorders include skin conditions caused by *P. acnes*, hypersensitivity, acne, folliculitis and endophthalmitis. *P. acnes* is also involved in infections of bone, joints and the central nervous system. However, it is particularly important to treat *P. acnes* infections associated with acne vulgaris. A method for detecting the presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the infection and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note, the sequence data for this patient did not form part of the patient specification, but was obtained in electronic format directly from WIPO at <http://www.wipo.int/patdb/patent.jsp?ref=US20010181581A2>.

XX
Sequence 378 AA:

query Match 100.0%; Score 31; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 2, Ac. 0%; Prec. No. 4, Cc. 0%;
Matches 6; Conservative 0; Mismatches 0; Gaps 0; Indels 0; Gaps 0;

XX
Sequence 755 AA:

query Match 100.0%; Score 31; DB 22; Length 755;
Best Local Similarity 100.0%; Pred. No. 3, Cc. 0%;
Matches 6; Conservative 0; Mismatches 0; Gaps 0; Indels 0; Gaps 0;

QY	1 Vorkgr 6	11111	14-JUL-1996	(first entry)
DB	303 Vorkgr 408			
RESULT	8			
ID	AAY07728			
AAV07728 standard protein.	118 AA.			
AI*	AAY07728;			
XX				
AI*	AAY07728;			
XX				
DE	Armenian hamster alpha-1 integrin subunit protein.			
XX				
KW	VEGF; tumour angiogenesis inhibitor; vascular endothelial growth factor;			
KW	endothelial cell surface receptor; capillary; blood vessel; hamster;			
KW	alpha-1 subunit; alpha-2 subunit;			
QS	capillulas mutatorius.			
XX				
QS	WO991645; Al.			
XX				
PR	01 APR 1996.			
PD	01 SEP 1997; 97W0-US17485.			
PP	30 SEP 1997; 97W0-US17485.			
PR	01 SEP 1997; 97W0-US17485.			
XX				
PA	(BETH-) BETH ISRAEL DEACNESS MEDICAL CENT.			
PA	(CLAEF/ CLAFER K. P.			
PA	(DETM/ DETMAR M.			
PA	(SENG/ SENGIER D. R.			
PA	Claefter KP, Detmar M, Sengier DR;			
PS	DISCLOSURE: FIG 2A-C; 6APP; English.			
PR	14-JUL-1996; 251930; 21			
XX				
PT	Inhibition of tumor angiogenesis through interaction of vascular endothelial growth factor and integrin cell surface receptors.			
CC	This invention describes a novel method for the inhibition of tumour angiogenesis mediated by vascular endothelial growth factor (VEGF) and integrin cell surface receptors expressed in vasculature of living subjects. The method inhibits new capillary and new blood vessel formation both within a tumour mass itself as well as in the immediately adjacent blood vasculature surrounding the periphery of the tumour mass. This interaction and dependence upon VEGF to induce specific interactions, however, in tumour angiogenesis, and unlike prior art, relies on the specific inter relationship of VEGF and integrins, rather than the concentrating solely on one specific class of protein.			
XX				
SQ	Sequence 1 184 AA;			
XX				
Query Match	100.0%	Score: 31; 142 20; Length: 118 8;	96.98%	Score: 402; 198 17; Length: 67;
Best Local Similarity	100.0%	Pred.: No. 6, 86, 0.2;	93.98%	Pred.: No. 4, 43;
Matches	6;	Mismatches: 0;	1;	Mismatches: 0;
CC	conservative	Indels: 0;	64ps	64ps
QY	1 Vorkgr 6	11111	14-JUL-1996	(first entry)
DB	242 Vorkgr 247			
RESULT	9			
ID	AAR87641			
AA887641 standard protein.	100 AA.			
XX				
AI*	AA887641;			
XX				
DE	Reported sequence shown open reading frame protein sequence SEQ ID NO: 24.			
XX				

comarchaeum symbiosum; non-thermophilic; crenarchaeote; physiological laboratory; characterisation; archaea; therapeutic; industrial; laboratory; comarchaeum symbiosum.

WO200018909 A2
06-APR-2000.
29-SEP-1999; 99W01-US22752.
29-SEP-1999; 98US1-0142764
(DIVE-) DIVERSA CORP.
Swanson RV, Feldman RA, Schleper C;
WPI; Invn No: 2000018909 005
N-PSB; AAA55198.
New nucleic acids and proteins isolated from the non-thermophilic crenarchaeote *Comarchaeum symbiosum*, the nucleic acids and proteins identified in the present invention are useful in characterising the physiology of these archaea and can be used in therapeutic, industrial or laboratory techniques. AAA55186 to AAA55226 and AAy90913 to AAY90951 represent nucleic acids and proteins isolated from the non-thermophilic crenarchaeote *comarchaeum symbiosum*. The nucleic acids and proteins identified in the present invention are useful in characterising the physiology of these archaea and can be used in therapeutic, industrial or laboratory techniques. AAA55227 to AA55260 represent promoter sequences from *comarchaeum symbiosum*. AAA55261 to AA55265 represent fork primers and probes used in sequencing from the present invention.

Claim 267; page 143; 210pp; English.

AAA55186 to AAA55226 and AAy90913 to AAY90951 represent nucleic acids and proteins isolated from the non-thermophilic crenarchaeote *comarchaeum symbiosum*. The nucleic acids and proteins identified in the present invention are useful in characterising the physiology of these archaea and can be used in therapeutic, industrial or laboratory techniques. AAA55227 to AA55260 represent promoter sequences from *comarchaeum symbiosum*. AAA55261 to AA55265 represent fork primers and probes used in sequencing from the present invention.

Sequence 269 AA:
Query Match 96.89%; Score 30; 188 211; Length 269;
Best Local Similarity 83.39%; Pred 86 280-307; Cys 86; 280-307;
Matches 51; Conservative 11; Mismatches 0; Insertions 0; Deletions 0;
1 VAGGTP 6
55 IQRGR 60

SU11
Y90949
AAy90939 standard; Protein; 273 AA.
AAy90949;
30-AUG-2000 (first entry)

comarchaeum symbiosum open reading frame; protein sequence; SEQ ID NO:5
comarchaeum symbiosum; non-thermophilic; crenarchaeote; physiological laboratory; characterisation; archaea; therapeutic; industrial; laboratory; comarchaeum symbiosum.

WO200018909 A2.
06-APR-2000.
29-SEP-1999; 99W01-US22752.
(DIVE-) DIVERSA CORP.
Swanson RV, Feldman RA, Schleper C;

(d) wound healing; (e) neurological diseases e.g., cerebral anoxia and epiphysis; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://ipo.int/pup/published_pct_sequences.

Sequence 64 AA:

Query Match 90.3%; Score 28; DB 91; length 64;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservation 1; Mismatch 0; InDel 0; Caps 0;
 QY 1 Voposp 6
 DB 18 VERGSR 24
 RESULT 13
 AAPB1759 standard; protein: 145 AA.
 ID AAPB1759 standard; protein: 145 AA.
 AC AAPB1759,
 XX
 DT 15-NOV-1990 (first entry)
 DE Sequence encoded by env gene of SIV-1 (continued from P81768).
 XX
 KW AIDS; immunogen; antigen; vaccine; diagnostic;
 XX
 OS Simian immunodeficiency virus.
 PN W0805440-A.
 XX
 PD 28-JUL-1988.
 XX
 PF 15 JAN 1988; 89W01-FB00025;
 PR 15 APR 1987; 87FR-0005398
 PA (INSP) INST PASTEUR (A17.2)
 PA Allion M, Montanier L, Guetard P, Clavill F, Sonigo P, Guyader M,
 PI Tiofais P, Chakrabarti L, Desoete R,
 XX
 WP1: 1988-22/129/41.
 IN-PDB: AANB0860.

New peptide(s) with immunological properties of HIV-2 envelope protein having the structure of simian immune deficiency virus proteins, useful in diagnosis and of vaccine components.

Disclosure: Fig 1B; 86pp; French.

XX New peptides with immunological properties of HIV-2 and also have a peptide backbone of the envelope protein of HIV-2 and also have a peptide structure in common with that of SIV1 glycoprotein are claimed. Antigenic and immunogenic conjugates coated, the peptides and a kit to detect HIV-2 in biological fluids are new, the peptides are useful for in vitro diagnosis of HIV-2 infection and some of them can be used as components on immunoplates and vaccines against HIV-2 antibodies against them can be used for treatment of AIDS.

Sequence 145 AA:

Query Match 90.4%; Score 28; DB 91; length 145;
 Best Local Similarity 84.3%; Pred. No. 2.8e+02;
 Matches 5; Conservation 1; Mismatch 0; InDel 0; Caps 0;
 QY 1 Voposp 6
 DB 122 LQGRGR 127

RESULT 14
AAPB1759 standard; protein: 212 AA.

ID AAPB1759
 XX
 KW Human secreted protein; gene therapy; protein; tissue; cancer;
 KW tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS;
 KW developmental abnormality; facial deformity; Alzheimer's disease;
 KW cognitive disorder; schizophrenia; immunological disorder; mood disorder;
 KW haematoopoietic disease; respiratory disorder; arthritis; skeletal; cardiovascular disorder; neural; osteoporosis; metabolic disorders;
 KW endocrine; asthma; intestinal; asterointestinal; diagnosis.
 XX Homo sapiens.
 XX
 PN W0901129-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 40-JUN-1998; 98W010814608.
 XX
 PR 12-SEP-1997; 97US-0053663.
 PR 01-JUL-1997; 97US-0051081.
 PR 01-JUL-1997; 97US-0051480.
 PR 12-SEP-1997; 97US-005398.
 XX
 PA (HUMAN) HUMAN GENOME SCI INC.
 XX
 PA Carter KJ, Hinchliff GA, Peng P, Kostoff CA, Rabkin SM;
 XX
 PR 1999-10622/094.
 PR W1999-10622/094.
 PR W1999-10622/094.
 XX
 PT New isolated human genes and the secreted polypeptides they encode.
 PT isolated human genes and truncated fragments thereof, human
 PT disorders, immune diseases, immune deficiency diseases or blood
 PT disorders.
 XX
 Disclosure: page 27; 179pp; English.
 XX
 CC The invention relates to nucleic acid sequences (AAPB1759 to AAPB2243) encoding human secreted proteins (AY01135 to AY01158). The secreted proteins in gene sequences are deposited with the Alice under deposit number AY01135-18. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for therapeutic, treatment or ameliorating medical conditions or by protein or gene therapy. Pathological conditions can be treated, diagnosed and determined by determining the amount of the new polypeptides. Specific uses are described for each of the new polypeptides, based on which diseases they are most likely expressed. The new polypeptides can be used for the diagnosis or treatment of cancer, diabetes, developmental abnormalities and total deficiencies, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, schizophrenia, immunological disorders, immune deficiency diseases (AIDS), mood disorders, respiratory disorders, arthritis, asthma, haemopoietic, neural disorders, skeletal disorders, endocrinological disorders or osteoporosis, metabolic disorders, cardiovascular disorders, disorders of gastrointestinal disorders. The present sequence represents a peptide to treat their blighted patients. The present sequence represents a peptide to treat encoded by a gene of the invention (see descriptive line for gene number).

XX Sequence 212 AA:
 SQ Query Match 90.4%; Score 28; DB 91; length 212;

Best local similarity 0.38; Pred. No. 0.402; Length 144; Seq: Msmatohs

Matches 5; Conservative: 1; Mismatchs: 0; Insertions: 0; Deletions: 0;

The auto_Fcode is used in a composite for suppressing autoimmune disease when administered to a mammal in a therapeutic effective amount.

XX lesions are oral in monkey, cat, dog, rat, mouse.

Seq: Sequence: 347 AA:

```

Query Match: 99.9%; Score: 202 (8.12); Length: 347;
Best Local Similarity: 98.9%; Pred. No. 6.20.0.02;
Matches: 4; Insertions: 0; Deletions: 0; Gaps: 0;
CIGAR: 1 VQPLIE 4
ID: 149_VQPLIE_19.c

```

Start: Complicated; end:cat; Z: -2002; L: 0.02; O: 0;

Job time: 4.000000 seconds

RESULT 15

AARI5828 standard; protein: 247 AA.

XX

AI: AARI5828;

XX

DT: 12 MAY 1992 (first entry)

DE: Modified ET, specific serCR, serCR.

XX

KW: Fluorescent; single chain; T-cell receptor; autoimmune disease.

XS: Homo sapiens.

XX

Key

FT: domain

FT: domain

FT: domain

FT: domain

FT: Receptor

FT: Misc-difference 10

FT: Misc-difference 10

FT: Misc-difference 41

FT: Misc-difference 41

FT: Misc-difference 111

FT: Misc-difference 111

FT: Misc-difference 152

FT: Misc-difference 152

FT: Misc-difference 146

FT: Misc-difference 146

XX

FN: W911801-A.

XX

PO: 2B NEW-1991.

PP: 10 MAY 1991; 91W0-4504284

PR: 15 MAY 1990; 90HS-6.2.3632.

XX

PA: (S901) SOUTHERN INSTITUTE,

PA: (S901) TANA PARKER CANCER INST.

XX

PI: Reinherz El.; Novotny J.; Smiley ST; Li P.; Ganju R;

DR: WPI: 1991-46188/50.

DR: NSUB: AAQ1500H.

XX

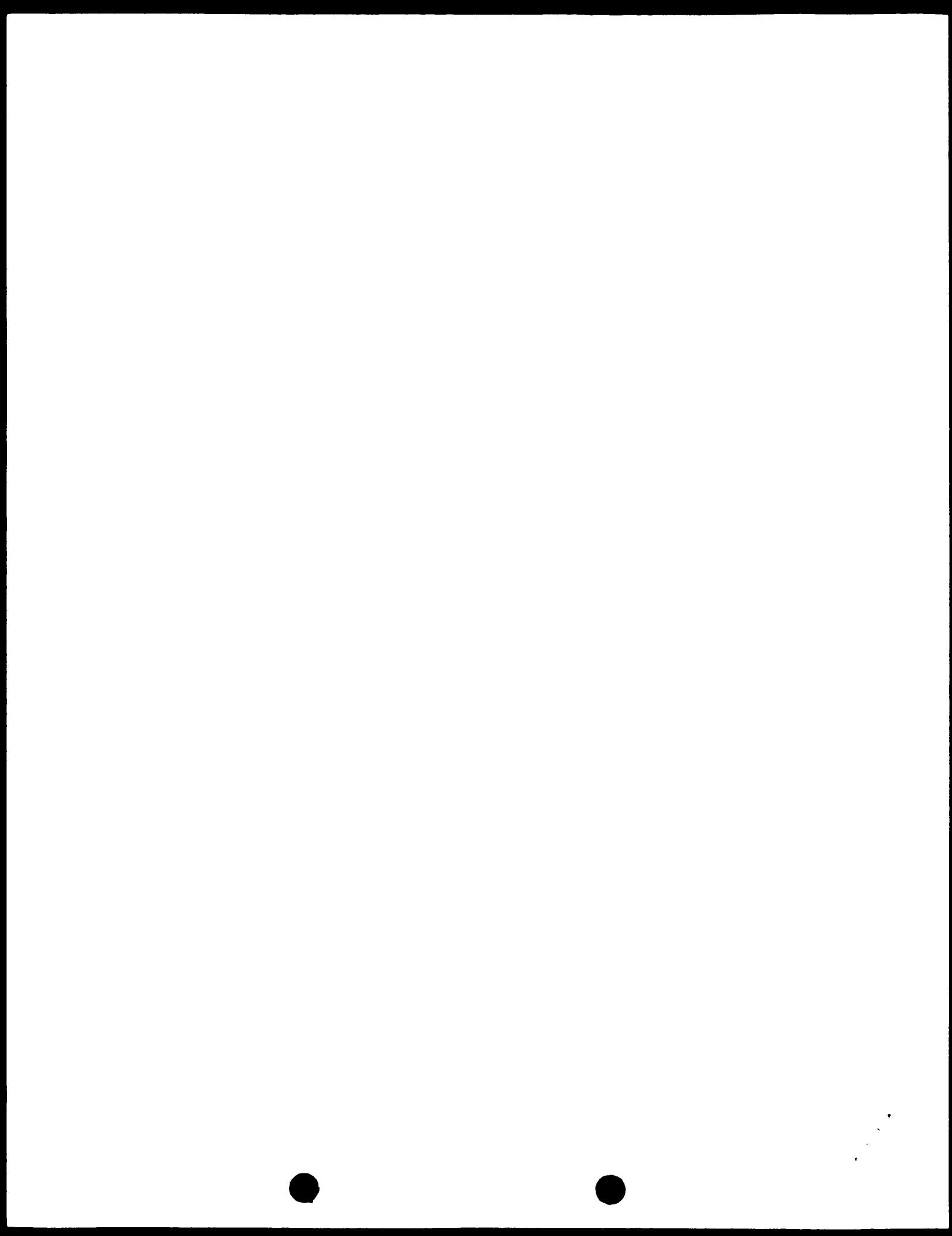
New soluble single chain T-cell receptors useful in suppression of and diagnostic autoimmune disease by binding specific antigenic complexes and treating infectious diseases.

XX

PS: Example 2; page 42; lang: English.

XX

To increase the solubility of the soluble anti-fluorescein antibody as in Arg1529 and Asn15507, a number of hydrophobic variable region amino acid residues predicted to be surface-exposed were replaced with more hydrophilic amino acid residues, as indicated in the features. The sequence (Arg1568) encoding this protein was subsectioned into the pSS1 secretion vector, which has the polylinker



RESULT 2
OS-09-342-084-11
Sequence 11: Application US/09-442084
Patent No. 6251668

GENERAL INFORMATION:
APPLICANT: Calcon, Rebecca E.
ORGANISM: *Sakai, Hajime*
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-A
CURRENT APPLICATION NUMBER: 07/937,342-024
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/072,674
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 12
SEQ ID NO: 11
LENGTH: 266
TYPE: PRT
ORGANISM: *Mus musculus*
OS-09-342-084-11

Query Match: 87.1% Score: 27; 139 121 163 211 257;
best local similarity: 100.0%; Pred. No.: 342-024
Matches: 5; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 2 Q9GR 6
Db 19 1111
Dc 19 Q9GR 24

RESULT 3
OS-09-342-094-2
Sequence 2: Application US/09-442084
Patent No. 6251668

GENERAL INFORMATION:
APPLICANT: Calcon, Rebecca E.
ORGANISM: *Sakai, Hajime*
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-A
CURRENT APPLICATION NUMBER: 07/937,342-084
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/072,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO: 2

Query Match: 87.1% Score: 27; 139 121 163 211 257;
best local similarity: 100.0%; Pred. No.: 342-024
Matches: 5; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 2 Q9GR 6
Db 212 Q9GR 216

RESULT 4
OS-09-342-084-2
Sequence 8: Application US/0869184B
Patent No. 598218
GENERAL INFORMATION:
APPLICANT: Tomasetto, Catherine
APPLICANT: Bazzet, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Sequences Comprising
TITLE OF INVENTION: *α-Lactokinin Receptor Subunit Proteins*

NUMBER OF SEQUENCES: 124
COUNTRY/STATE/CITY: USA
ADDRESS: Sternen, Rosseter, Goldstein & Fox P.L.L.C.,
STREET: 11th New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-0934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
LOADING DEVICE: PC-520 MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
TITLE OF INVENTION: DATA
APPLICANT NUMBER: 07/937,342-024-024
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
APPLICATION NUMBER: 09-AUG-1996
FILING DATE: 09-AUG-1996
ATTORNEY/AGENT: REINHOLD, GMBH
NAME: Stein, Eric K.
REGISTRATION NUMBER: 36,698
REFERENCE NUMBER: 1483,0090001
TITLE: IDENTIFICATION OF A PROTEIN
TELEPHONE: 292-271-2600
TELEFAX: 202-371-2543
THE MATCHES ARE SEQ ID NO: 8;
SEQUENCE CHARACTERISTICS:
LURCHI, 534 amino acids
TYPE: amino acid
SEQUENCE: Linear
MOLECULE TYPE: protein
US 08 691 014B 8

Query Match: 87.1% Score: 27; 139 121 163 211 257;
best local similarity: 100.0%; Pred. No.: 598218
Matches: 0; Mismatches: 0; Gaps: 0;

QY 2 Q9GR 6
Db 51 Q9GR 55

RESULT 5
US 08 630 172 9
Sequence 9: Application US/0869184B
Patent No. 598054
GENERAL INFORMATION:
APPLICANT: Shantz, Ober
TITLE OF INVENTION: KAVALLIS-KAOGUT AND FvorESS FOR T
NUMBER OF SEQUENCES: 41
COUNTRY/STATE/CITY: USA
ADDRESS: Sternen, Rosseter, Goldstein & Fox P.L.L.C.,
STREET: 11th New York Ave., NW, Suite 600
CITY: Washington
STATE: District of Columbia
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
LOADING DEVICE: PC-520 MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: 07/937,342-024
FILING DATE: 31-JUL-1996
CLASSIFICATION: 514
ATTORNEY/AGENT: INFORMATION
NAME: Connelly, Gary J.
REGISTERED NUMBER: 33/39730-172
FILING DATE: 22-JUL-2000
SEQUENCE NUMBER: 2879-36

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 863-9740
 TELEFAX: (404) 963-0223
 INFORMATION FOR SEQ ID NO: 9;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1065 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SOURCE Match: S 09 475-419 9
 Best Local Similarity: 190.0%
 Matches: 67; conservative: 0;
 i) 2 ORGANIC
 f) 111
 o) 465 ORGANIC 469

SOURCE Match: S 09 475-419 9
 Best Local Similarity: 190.0%
 Matches: 67; conservative: 0;
 i) 2 ORGANIC 6
 f) 111
 o) 465 ORGANIC 469

SOURCE Match: S 09 475-419 9
 Best Local Similarity: 190.0%
 Matches: 67; conservative: 0;

DS 08-78-078	2	Stephanie	Stephanie	Information	DS 08-78-078
APPLICANT:	Patent No. 6,044,066				
GENERAL INFORMATION:					
APPLICANT:	Benedict, Stephen H.				
APPLICANT:	Silvana, Verena				
APPLICANT:	McGinn, Marcia				
APPLICANT:	Scott, Robert L.				
NAME OF INVENTOR:	STAN LIZIA & STEPHEN H. MCGINN				
NAME OF INVENTOR:	THOMAS T. TAKAHASHI				
NUMBER OF SPECIMENS:	19				
CABINET'S BUREAU ADDRESS:	AGRICULTURAL HIGHWAY, WILLIAMS, CALIFORNIA & COLLINS				
STREET:	1101 WALNUT ST.				
CITY:	Kansas City				
STATE:	Mo.				
COUNTRY:	USA				
ZIP CODE:	64106				
086 OTHER RELIABLE FORM:					
RELEASER TYPE:	FLOPPY DISK				
COMPUTER: IBM PC compatible					
OPERATING SYSTEM:	WINDOWS/MACINTOSH				
SOFTWARE:	Frontend for Release #1.0, Version #1.25				
OTHER INFORMATION DATA:					
APPENDIX DATA: R09636, G09637A6, S78					
FILING DATE: 03-FEB-1997					
ASSIGNMENT LINE: 51A					
PRIOR APPLICATION DATA:					
ATTACHMENT NUMBER: 008/229, 51A					
FILED DATE: 19-AUG-1994					
APPLICANT/INVENTOR INFORMATION:					
NAME: SCILLING, ROBIN M.					
RESIDENCE NUMBER: 26262					
REFERENCE/DOC ID NUMBER: 22884					
TELEPHONE NUMBER: (816)474-9950					
FAX: (816)474-9057					
THEX: 4-44 46,3					
SEQUENCE CHARACTERISTICS:					
LENGTH: 1170 amino acids					
TYPE: alpha-acid					
TOPOLACY: linear					
MOLECULE TYPE: Protein					
HYPOTHETICAL: No					
ORIGINAL SOURCE:					
ORGANISM: Homo sapiens					
CELL TYPE: T-cell					
CELL LINE: HL60					
FEATURE:					
SEQUENCE: Position					
POSITION: 1-1175					
OTHER INFORMATION: /label signal					
OTHER INFORMATION: /note "Signal sequence"					
FEATURE:					
NAME/KEY: Position					
LOCATION: 1-1175					
OTHER INFORMATION: /label Repeat					
OTHER INFORMATION: /note "Repeat 1"					
FEATURE:					
NAME/KEY: Position					
LOCATION: 1-1175					
OTHER INFORMATION: /label Repeat					
OTHER INFORMATION: /note "Repeat 1"					
FEATURE:					
NAME/KEY: Position					
LOCATION: 1-1175					
OTHER INFORMATION: /label Repeat					
OTHER INFORMATION: /note "Label Repeat"					

OTHER INFORMATION: "Notes" "Repeat" "V"

FEATURE:
NAME/KEY: Relation
LOCATION: 447-529
OTHER INFORMATION: /label= "Repeat"
/notes= "Repeat V"

FEATURE:
NAME/KEY: Relation
LOCATION: 509-547
OTHER INFORMATION: /label= "Repeat"
/notes= "Repeat V"

FEATURE:
NAME/KEY: Relation
LOCATION: 568-629
OTHER INFORMATION: /label= "Repeat"
/notes= "Repeat V"

FEATURE:
NAME/KEY: Found in
LOCATION: 170-176
OTHER INFORMATION: /label= "Transmembrane domain"
/notes= "1 domain"

FEATURE:
NAME/KEY: Domain
LOCATION: 1089-1112
OTHER INFORMATION: /label= "Transmembrane domain"
/notes= "Transmembrane domain"

FEATURE:
NAME/KEY: Power
LOCATION: 1113-1176
OTHER INFORMATION: /label= "Cytoplasmic domain"
/notes= "Cytoplasmic domain"

PUBLICATION INFORMATION:
AUTHORS: Piroozi,
TITLE: LFA-1 Amino acid sequence (alpha1) chain
TITLE: PMA-stimulated HL-60 cells
JOURNAL: The Adhesion Molecule
PAGES: 94-95
DATE: 1993

RELEVANT REFERENCES IN 3DZ: 14 Nov. 2000 EMBL 173715

US-08-739 078-2

RESULT 8

Query Match 87.1% Score 27: DB 27 Length 1170;
Best Local Similarity 99.6% Fred. 63.1 Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 DRRGR 6
1b 483 DRGR 453

US-08-732-634-2

Scopus 2; Application 03/09/2003
Patent No.: 6,563,866
GENERAL INFORMATION:
APPLICANT: Becegis, Stephan H.
APPLICANT: Stadlauer, Veronika
APPLICANT: Chanc, Maria
APPLICANT: Tibellus, Groett
TITLE OF INVENTION: CAR LYZA 1 PROTEIN FOR PHAGOCYTES
NUMBER OF SEQUENCES: 19
SEQUENCE ALIGNMENT:
ADDRESSEE: Avery, William, 1399 45th & Main St.
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64136
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OTHER INFORMATION: "Notes" "Repeat V"

SOFTWARE: PatentIn Release #1.0, Version #1.25

WORKING APPLICATION DATA:
ACTIVE/INACTIVE: Member, 23/08/2003
FILED DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collette, John M.
RATES/TRAITS: MEMBER, 24/24/2
FEE AGREEMENT: FEE AGREEMENT, 24/24
FAX: 312-341-1333; FAX: 312-341-1331;
TELEPHONE: (847)471-5050
TELEFAX: (847)471-9057

TELEX: 434-163

INFORMATION FOR SEQ ID NO: 2:

SIMILARITY CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
TOPOLogy: linear
BIOLOGICAL FUNCTION: Protein
HYBRIDIZATIONAL: No
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

CELL TYPE: U-251
CELL LINE: U-251

FEATURE:
NAME/KEY: Region
LOCATION: 1-25
OTHER INFORMATION: /label= "Signal sequence"
FEATURE:
NAME/KEY: Region
LOCATION: 32-79
OTHER INFORMATION: /label= "Repeat I"
FEATURE:
NAME/KEY: Region
LOCATION: 349-519
OTHER INFORMATION: /label= "Repeat II"
FEATURE:
NAME/KEY: Region
LOCATION: 519-641
OTHER INFORMATION: /label= "Repeat III"
FEATURE:
NAME/KEY: Region
LOCATION: 642-742
OTHER INFORMATION: /label= "Repeat IV"
FEATURE:
NAME/KEY: Region
LOCATION: 743-753
OTHER INFORMATION: /label= "Repeat V"

FEATURE:
NAME/KEY: Region
LOCATION: 744-754
OTHER INFORMATION: /label= "Repeat VI"

FEATURE:
NAME/KEY: Region
LOCATION: 755-765
OTHER INFORMATION: /label= "Repeat VII"

FEATURE:
NAME/KEY: Region
LOCATION: 766-776
OTHER INFORMATION: /label= "Repeat VIII"

FEATURE:
NAME/KEY: Region
LOCATION: 777-787
OTHER INFORMATION: /label= "Repeat IX"

FEATURE:
NAME/KEY: Region
LOCATION: 788-798
OTHER INFORMATION: /label= "Repeat X"

OTHER INFORMATION: /take 1 trans.
 OTHER INFORMATION: /take 1 trans.
 PRACTICE: *bioactive materials technology*
 NAME/KEY: domain
 LOCATION: 1113-1170
 OTHER INFORMATION: /take 1 bioactive materials technology
 PUBLICATION INFORMATION:
 AUTHORS: picot,
 power,
 TITLE: LFA-1 Amino acid sequence (cDNA) (1113-
 1170)
 PMA-stimulated IL-60 events)
 JOURNAL: The Adhesion Molecule Facts Book
 PAGES: 94-95
 DATE: 1994
 RELEVANT REFERENCES: IN SP2 1113-1170
 88-08-752-64-2
 88-08-676-062A-42
 88-08-676-062A-42
 88-08-676-062A-42
 Sequence 4.2, Application: 98/0847606.2A
 Patent No. 5,877,275
 GENERAL INFORMATION:
 APPLICANT: Arthrogen, Inc., Ann Arbor, MI
 TITLE OF INVENTION: COMMERCIAL CELLULAR IMMUNOTHERAPY
 TITLE OF INVENTION: RESPONSES WITH BETA2 INTTEGRINS
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish, S Richardson, Ph.D.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: EAST-SEA for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/0847606.2A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/216,081
 FILING DATE: 21-MAR-1994
 APPLICATION NUMBER: 08/104,783
 FILING DATE: 04-JAN-1994
 APPLICATION NUMBER: 07/509,842
 FILING DATE: 14-JUN-1990
 APPLICATION NUMBER: 07/212,573
 FILING DATE: 28-JUN-1998
 ATTORNEY: ANDREW M. WATKINS
 NAME: Frederick, John W.
 REGISTRATION NUMBER: 29,016
 REFERENCE/EXCETION INFORMATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-8906
 TELEFAX: 201/542-4242
 INFORMATION FOR SEQ ID NO: 1
 INFORMATION CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

14
 5 09-564-805 244
 Sequence 245, Application US/09564805
 Patent No. 6,434,038
 GENERAL INFORMATION:
 APPLICANT: Tavt et al., Sean V.
 APPLICANT: Teng, David H.F.
 APPLICANT: Simard, Jacques
 APPLICANT: Rommens, Johanna M.
 APPLICANT: Myriad Genetics, Inc.
 TITLE OF INVENTION: Gene and a Panel
 FILE REFERENCE: 2418-25B
 CURRENT APPLICATION NUMBER: US67047664
 CURRENT FILING DATE: 2000-05-05
 PRIOR APPLICATION NUMBER: US 60/107,
 PRIOR FILING DATE: 1998-11-06
 PRIOR FILING DATE: 1999-11-05
 NUMBER OF SEQ ID NOS: 240
 SOFTWARE: Patch It Ver. 2.0
 SEQ ID NO: 244
 LENGTH: 684
 TYPE: PRT
 ORGANISM: Homo sapiens
 5 09-564-805 244
 Query Match 83.9% Score:
 Best Local Similarity 83.3% Predicted:
 Matches 5; Conservative 0; Miss:
 1 VNRAGR 6
 1 1 1 1
 2 30 VNRAGR 245

